The cDNAs of the invention also enable cells transfected or transformed with expression vectors driving the expression of the encoded polypeptides and antibodies reactive with the polypeptides.

[070] In one embodiment, the invention provides for isolated polypeptides, preferably, pine tree polypeptides. As used herein, the term "polypeptides" refers to a genus of polypeptide or peptide fragments that encompass the amino acid sequences identified from Table I, as well as smaller fragments. Consequently, the invention encompasses any polypeptide fragment comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 contiguous amino acids encoded by the cDNAs of any of SEQ ID NOS: 1-327, or comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 contiguous amino acids of any of amino acid sequence derived from Table I.

[071] Alternatively, a polypeptide may be defined in terms of its antigenic relatedness to any peptide encoded by SEQ ID NOS: 1-327. Thus, in one embodiment, a polypeptide within the scope of the invention is defined as an amino acid sequence comprising a linear or 3-dimensional epitope shared with any peptide encoded by the cDNAs of SEQ ID NOS: 1-327. Alternatively, a polypeptide within the scope of the invention is recognized by an antibody that specifically recognizes any peptide encoded by SEQ ID NOS: 1-327. Antibodies are defined to be specifically binding if they bind pine tree polypeptides with a K_a of greater than or equal to about 10^7 M^{-1}, and preferably greater than or equal to 10^8 M^{-1}.

[072] A polypeptide "variant" as referred to herein means a polypeptide substantially homologous to a native polypeptide, but which has an amino acid sequence different from that encoded by any of SEQ ID NOS: 1-327 because of one or

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more deletions, insertions or substitutions. The variant amino acid sequence preferably is at least 80% identical to a native polypeptide amino acid sequence, preferably at least 90%, more preferably, at least 95% identical over at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21-25, or 26-30 contiguous amino acids. The percent identity between an amino acid sequence encoded by any of SEQ ID NOS: 1-327 and a potential variant can be determined manually, or, for example, by comparing sequence information using the GAP computer program, version 6.0 described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) and available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program, described above, utilizes the alignment method of Needleman and Wunsch (*J. Mol. Biol.* 48:443,1970), as revised by Smith and Waterman (*Adv. Appl. Math* 2:482,1981).

[073] Variants can comprise conservatively substituted sequences, meaning that a given amino acid residue is replaced by a residue having similar physiochemical characteristics. Examples of conservative substitutions include substitution of one aliphatic residue for another, such as Ile, Val, Leu, or Ala for one another, or substitutions of one polar residue for another, such as between Lys and Arg; Glu and Asp; or Gln and Asn. See Zubay, Biochemistry, Addison-Wesley Pub. Co., (1983) incorporated by reference in its entirety. The effects of such substitutions can be calculated using substitution score matrices such a PAM-120, PAM-200, and PAM-250 as discussed in Altschul, (*J. Mol. Bio*l. 219:555-65, 1991). Other such conservative substitutions, for example, substitutions of entire regions having similar hydrophobicity characteristics, are well known.

[074] Naturally-occurring peptide variants are also encompassed by the invention. Examples of such variants are proteins that result from alternate mRNA splicing events or from proteolytic cleavage of the polypeptides of Table I. Variations attributable to proteolysis include, for example, differences in the N- or C-termini upon expression in different types of host cells, due to proteolytic removal of one or more terminal amino acids from the polypeptides encoded by the sequences of Table I (generally from 1-5 terminal amino acids).

[075] As stated above, the invention provides recombinant and non-recombinant, isolated and purified polypeptides, preferably pine tree polypeptides. Variants and derivatives of native polypeptides can be obtained by isolating naturally-occurring variants, or the nucleotide sequence of variants, of other plant lines or species, or by artificially programming mutations of nucleotide sequences coding for native pine tree polypeptides. Alterations of the native amino acid sequence can be accomplished by any of a number of conventional methods. Mutations can be introduced at particular loci by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments of the native sequence. Following ligation, the resulting reconstructed sequence encodes an analog having the desired amino acid insertion, substitution, or deletion. Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered gene wherein predetermined codons can be altered by substitution, deletion or insertion. Exemplary methods of making such alterations are discussed supra.